OIPE 0400
#5
Dmt
4-9-02

Serial Number: 10/040,803 **ENTERED**

CRF Processing Date: 1/30/2002
Edited by: _____
Verified by: ___/s/___ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII.

- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- ☐ Edited a format error in the Current Application Data section, specifically: 1652
  _____

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

- ☐ Added the mandatory heading and subheadings for "Current Application Data".

RECEIVED

- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

APR 0 3 2002

- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

TECH CENTER 1600/2900
  _____

- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
  _____

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
  _____

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- ☐ Inserted colons after headings/subheadings. Headings edited included:
  _____

- ☐ Deleted extra, invalid, headings used by an applicant, specifically:
  _____

- ☑ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____.

- ☐ Inserted mandatory headings, specifically: _____

- ☐ Corrected an obvious error in the response, specifically:
  _____

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

- ☐ Corrected an error in the Number of Sequences field, specifically:
  _____

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- ☐ Other:
  _____
  _____
  _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.   3/1/95

RAW SEQUENCE LISTING   DATE: 01/30/2002
PATENT APPLICATION: US/10/040,803   TIME: 20:34:50

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\01302002\J040803.raw

```
    2 <110> APPLICANT: Andrade-Gordon, Patricia
    3         Darrow, Andrew L.
    4         Qi, Jenson
    6 <120> TITLE OF INVENTION: DNA encoding human serine protease C-E
    8 <130> FILE REFERENCE: ORT-1030
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/040,803
C--> 11 <141> CURRENT FILING DATE: 2002-01-07
   13 <160> NUMBER OF SEQ ID NOS: 11
   15 <170> SOFTWARE: PatentIn Ver. 2.0
   17 <210> SEQ ID NO: 1
   18 <211> LENGTH: 1430
   19 <212> TYPE: DNA
   20 <213> ORGANISM: Homo sapiens
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   24 gcatcgccct gggtctctcg agcctgctgc ctgctccccc gccccaccag ccatggtggt 120
   25 ttctggagcg cccccagccc tgggtggggg ctgtctcggc accttcacct ccctgctgct 180
   26 gctggcgtcg acagccatcc tcaatgcggc caggatacct gttcccccag cctgtgggaa 240
   27 gccccagcag ctgaaccggg ttgtgggcgg cgaggacagc actgacagcg agtggccctg 300
   28 gatcgtgagc atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 360
   29 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat acctgttctc 420
   30 tgtgctgctg ggggcctggc agctggggaa ccctggctct cggtcccaga aggtgggtgt 480
   31 tgcctgggtg gagccccacc ctgtgtattc ctggaaggaa ggtgcctgtg cagacattgc 540
   32 cctggtgcgt ctcgagcgct ccatacagtt ctcagagcgg gtcctgccca tctgcctacc 600
   33 tgatgcctct atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 660
   34 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg ttcctatcat 720
   35 cgactcggaa gtctgcagcc atctgtactg gcggggagca ggacagggac ccatcactga 780
   36 ggacatgctg tgtgccggct acttggaggg ggagcgggat gcttgtctgg gcgactccgg 840
   37 gggcccccctc atgtgccagg tggacggcgc ctggctgctg gccggcatca tcagctgggg 900
   38 cgagggctgt gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccgctc 960
   39 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg ggggtggggc 1020
   40 cctcagggca ccgagccagg gctctggggc cgccgcgcgc tcctagggcg cagcgggacg 1080
   41 cggggctcgg atctgaaagg cggccagatc cagatctgga tctggatctg cggcggcctc 1140
   42 gggcggtttc ccccgccgta aataggctca tctacctcta cctctggggg cccggacggc 1200
   43 tgctgcggaa aggaaacccc ctccccgacc cgcccgacgg cctcaggccc cgcctccaag 1260
   44 gcatcaggcc ccgcccaacg gcctcatgtc cccgccccca cgacttccgg ccccgccccc 1320
   45 gggccccagc gcttttgtgt atataaatgt taatgatttt tataggtatt tgtaaccctg 1380
   46 cccacatatc ttatttattc ctccaatttc aataaattat ttattctcca         1430
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   49 <211> LENGTH: 1166
   50 <212> TYPE: DNA
   51 <213> ORGANISM: Artificial Sequence
   53 <220> FEATURE:
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54 <223> OTHER INFORMATION: Description of Artificial Sequence: C-E catalytic
55       domain in a zymogen activated construct
57 <400> SEQUENCE: 2
58 gaattcacca ccatggacag caaaggttcg tcgcagaaat cccgcctgct cctgctgctg 60
59 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga cgacgacgac 120
60 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tggggggctat 180
61 gctctagagg acagcgagtg gccctggatc gtgagcatcc agaagaatgg gacccaccac 240
62 tgcgcaggtt ctctgctcac cagccgctgg gtgatcactg ctgcccactg tttcaaggac 300
63 aacctgaaca aaccatacct gttctctgtg ctgctggggg cctggcagct ggggaaccct 360
64 ggctctcggt cccagaaggt gggtgttgcc tgggtggagc cccaccctgt gtattcctgg 420
65 aaggaaggtg cctgtgcaga cattgccctg gtgcgtctcg agcgctccat acagttctca 480
66 gagcgggtcc tgcccatctg cctacctgat gcctctatcc acctccctcc aaacacccac 540
67 tgctggatct caggctgggg gagcatccaa gatggagttc ccttgcccca ccctcagacc 600
68 ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct gcagccatct gtactggcgg 660
69 ggagcaggac agggacccat cactgaggac atgctgtgtg ccggctactt ggagggggag 720
70 cgggatgctt gtctgggcga ctccgggggc cccctcatgt gccaggtgga cggcgcctgg 780
71 ctgctggccg gcatcatcag ctggggcgag ggctgtgccg agcgcaacag gcccgggtc 840
72 tacatcagcc tctctgcgca ccgctcctgg gtggagaaga tcgtgcaagg ggtgcagctc 900
73 cgcgggcgcg ctcaggggg tggggccctc agggcaccga gccagggctc tggggccgcc 960
74 gcgcgctcct ctagacatca ccatcaccat cactagcggc cgcttcctt tagtgagggt 1020
75 taatgcttcg agcagacatg ataagataca ttgatgagtt tggacaaacc acaactagaa 1080
76 tgcagtgaaa aaaatgcttt atttgtgaaa tttgtgatgc tattgcttta tttgtaacca 1140
77 ttataagctg caataaacaa gttgac                                     1166
79 <210> SEQ ID NO: 3
80 <211> LENGTH: 22
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
86       oligonucleotide
88 <400> SEQUENCE: 3
89 ggataaaacc tggggcgacc tg                                        22
91 <210> SEQ ID NO: 4
92 <211> LENGTH: 24
93 <212> TYPE: DNA
94 <213> ORGANISM: Artificial Sequence
96 <220> FEATURE:
97 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
98       oligonucleotide
100 <400> SEQUENCE: 4
101 tccgggcccc cagaggtaga tgag                                      24
103 <210> SEQ ID NO: 5
104 <211> LENGTH: 20
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
110       oligonucleotide
112 <400> SEQUENCE: 5
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116 <211> LENGTH: 20
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
122       oligonucleotide
124 <400> SEQUENCE: 6
125 cagagaggct gatgtagacc                                          20
127 <210> SEQ ID NO: 7
128 <211> LENGTH: 317
129 <212> TYPE: PRT
130 <213> ORGANISM: Homo sapiens
132 <400> SEQUENCE: 7
133 Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly
134  1               5                  10                  15
136 Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala
137             20                  25                  30
139 Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn
140         35                  40                  45
142 Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile
143     50                  55                  60
145 Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu
146 65                  70                  75                  80
148 Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu
149             85                  90                  95
151 Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly
152             100                 105                 110
154 Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu Pro
155         115                 120                 125
157 His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala Leu
158     130                 135                 140
160 Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro Ile
161 145                 150                 155                 160
163 Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys Trp
164             165                 170                 175
166 Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro
167             180                 185                 190
169 Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys
170         195                 200                 205
172 Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp
173     210                 215                 220
175 Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
176 225                 230                 235                 240
178 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu Leu
179             245                 250                 255
181 Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg Pro
182             260                 265                 270
```

```
184 Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile
185          275              280              285
187 Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala Leu
188          290              295              300
190 Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala Arg Ser
191 305                  310              315
194 <210> SEQ ID NO: 8
195 <211> LENGTH: 327
196 <212> TYPE: PRT
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence: C-E catalytic
201        domain fusion protien
203 <400> SEQUENCE: 8
204 Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu Leu
205   1           5              10              15
207 Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
208          20              25              30
210 Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp
211          35              40              45
213 Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Asp Ser Glu Trp Pro
214          50              55              60
216 Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser
217   65              70              75              80
219 Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp
220              85              90              95
222 Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln
223          100             105             110
225 Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val
226          115             120             125
228 Glu Pro His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile
229          130             135             140
231 Ala Leu Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu
232 145             150             155             160
234 Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His
235              165             170             175
237 Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro
238          180             185             190
240 His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu
241          195             200             205
243 Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr
244          210             215             220
246 Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys
247 225             230             235             240
249 Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp
250              245             250             255
252 Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
253          260             265             270
255 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/040,803

DATE: 01/30/2002
TIME: 20:34:50

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\01302002\J040803.raw**

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256            275                280                285
258 Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly
259        290                295                300
261 Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala Arg Ser Ser
262 305                310                315                320
264 Arg His His His His His His
265                325
268 <210> SEQ ID NO: 9
269 <211> LENGTH: 40
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence: nested primer
275       oligonucleotide
277 <400> SEQUENCE: 9
278 ggacatgctg tgtgccggct acttggaggg ggagcgggat                      40
280 <210> SEQ ID NO: 10
281 <211> LENGTH: 33
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
287       oligonucleotide
289 <400> SEQUENCE: 10
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293 <211> LENGTH: 33
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
299       oligonucleotide
301 <400> SEQUENCE: 11
303 gtgctctaga ggagcgcgcg gcggccccag agc                             33
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VERIFICATION SUMMARY DATE: 01/30/2002
PATENT APPLICATION: US/10/040,803 TIME: 20:34:51

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\01302002\J040803.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date